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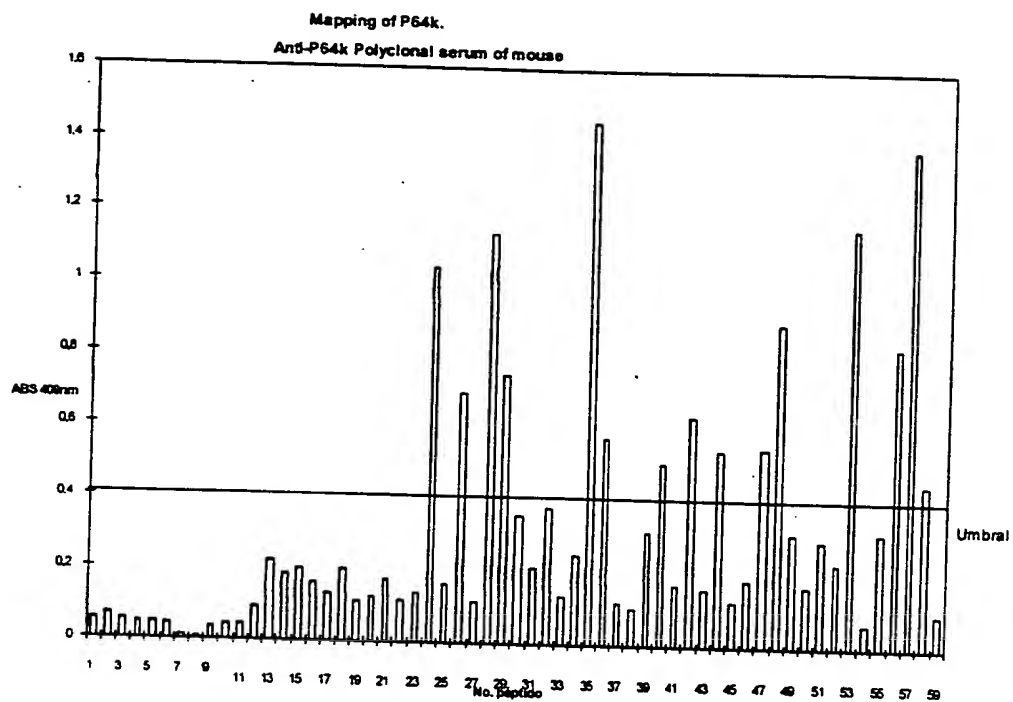
FIG. 1

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10	20	30	40	50	60	70
ATGCTAGATA	AAAGATGGC	TTTAGTTGAA	TTGAAAGTGC	CCGACATTGG	CGGACACGAA	AATGTAGATA
80	90	100	110	120	130	140
TTATCGCGGT	TGAAGTAAAC	GTGGGCGACA	CTATTGCTGT	GGACGATACC	CTGATTACTT	TGGAACCGA
150	160	170	180	190	200	210
TAAAGCGACT	ATGGACGTAC	CTGCTGAAGT	TGCAGGCGTA	GTCAAAGAAG	TAAAGTTAA	AGTCGGCGAC
220	230	240	250	260	270	280
AAAATCTCTG	AAGGTGGTTT	GATTGTCGTC	GTTGAAGCTG	AAGGCACGGC	AGCCGCTCCT	AAAGCCGAAG
290	300	310	320	330	340	350
CGGCTGCCGC	CCCGGCGCAA	GAAGCCCTA	AAGCTGCCGC	TCCTGCTCCG	CAAGCCGCGC	AATTCGGCGG
360	370	380	390	400	410	420
TTCTGCCGAT	GCCGAGTACG	ACGTGGTCGT	ATTGGGTGGC	GGTCCCGGCG	GTTACTCCGC	TGCATTGGCC
430	440	450	460	470	480	490
GCTGCCGATG	AAGGCTTGAA	AGTCGCCATC	GTCGAACGTT	ACAAAACCTT	GGGCGGCGTT	TGCCTGAACG
500	510	520	530	540	550	560
TCGGCTGTAT	CCCTTCCAAA	GCCTTGTTCG	ACAATGCCGC	CGTTATCGAC	GAAGTGCGCC	ACTTGGCTGC
570	580	590	600	610	620	630
CAACGGTATC	AAATACCCCG	AGCCGGAAC	CGACATCGAT	ATGCTTCGCG	CCTACAAAGA	CGGCGTAGTT
640	650	660	670	680	690	700
TCCCGCCTCA	CGGGCGGTTT	GGCAGGTATG	GCGAAAAGCC	GTAAAGTGGA	CGTTATCCAA	GGCGACGGGC
710	720	730	740	750	760	770
AATTCTTAGA	TCCGCACCAC	TTGGAAGTGT	CGCTGACTGC	CGGCGACGCG	TACGAACAGG	CAGCCCCTAC
780	790	800	810	820	830	840
CGGCGAGAAA	AAAATCGTTG	CCTTCAAAAA	CTGTATCATT	GCAGCAGGCA	GCCGCGTAAC	CAAACTGCCT
850	860	870	880	890	900	910
TTCATTCTCT	AAGATCCGCA	CATCATCGAT	TCCAGCGGCG	CATTGGCTCT	GAAAGAAGTA	CCGGGCAAAC
920	930	940	950	960	970	980
TGCTGATTAT	CGGCGGCGGC	ATTATCAGCC	TCGAGATGGG	TACGGTTTAC	AGCACGCTGG	GTTCCGCTTT
990	1000	1010	1020	1030	1040	1050
GGATGTGGTT	GAAATGATGG	ACGGCCTGAT	GCAAGGCGCA	GACCGCGATT	TGGTAAAAGT	ATGGCAAAAA
1060	1070	1080	1090	1100	1110	1120
CAAAACGAAT	ACCGTTTTGA	CAACATTATG	GTCACACCA	AAACCGTTGC	AGTTGAGCCG	AAAGAAGACG
1130	1140	1150	1160	1170	1180	1190
GCGTTTACGT	TACCTTTGAA	GGCGCGAACG	CGCCTAAAGA	GCCGCAACGC	TACGATGCCG	TATTGGTTGC
1200	1210	1220	1230	1240	1250	1260
CGCCGCGCCG	GCGCCCAACG	GCAAACATCAT	CAGCGCGGAA	AAAGCAGGCG	TTGCCGTAAC	CGATCGCGGC
1270	1280	1290	1300	1310	1320	1330
TTCATCGAAG	TGGACAAACA	AATGCGTACC	AATGTGCCGC	ACATCTACGC	CATCGCGCAC	ATCGTCGGTC
1340	1350	1360	1370	1380	1390	1400
AGCCGATGTT	GGCGCACAAA	GCCGTTACAG	AAGGCCACGT	TGCCGCCGAA	AACTGCGCCG	GCCACAAAGC
1410	1420	1430	1440	1450	1460	1470
CTACTTCGAC	GCACGCGTGA	TTCCGGGCGT	TGCCTACACT	TCCCCCGAAG	TGGCGTGGGT	GGGCGAAACC
1480	1490	1500	1510	1520	1530	1540
GAACTGTCCG	CCAAAGCCTC	CGGCGGCAAA	ATCACCAAAAG	CCAACTTCCC	GTGGGCGGCT	TCCGGCCGCTG
1550	1560	1570	1580	1590	1600	1610
CGATTGCCAA	CGGTTGCGAC	AACGGCTTTA	CCAAAGCTGAT	TTTTGATGCC	GAAACCGGCC	GCATCATCGG
1620	1630	1640	1650	1660	1670	1680
CGGCGGCATT	GTCGGTCCGA	ACGGTGGCGA	TATGATCGGC	GAAGTCTGCC	TTGCCATCGA	AATGGGCTGC
1690	1700	1710	1720	1730	1740	1750
GACGCGGCAG	ACATCGGCAA	AACCATCCAC	CCGCACCCGA	CCTTGGGCGA	ATCCATCGGT	ATGGCGGCGG
1760	1770	1780	1790	1797		
AAGTGGCATT	GGGTACTTGT	ACCGACCTGC	CTCCGCAAAA	GAAAAAA		

FIG. 2

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FIG. 3

5' TTCC⁴

			16			25			34			43			52					
M	V	D	K	R	M	A	L	V	E	L	K	V	P	D	I	G	G	H		
<u>ATG</u>	<u>GTA</u>	<u>GAT</u>	<u>AAA</u>	<u>AGA</u>	<u>ATG</u>	<u>GCT</u>	<u>TTA</u>	<u>GTT</u>	<u>GAA</u>	<u>TTG</u>	<u>AAA</u>	<u>GTG</u>	<u>CCC</u>	<u>GAC</u>	<u>ATT</u>	<u>GGC</u>	<u>GGA</u>	<u>CAC</u>		
61			70			79			88			97			106			115		
E	N	V	D	I	I	A	V	E	V	N	V	G	D	T	I	A	V	D		
<u>GAA</u>	<u>AAT</u>	<u>GTA</u>	<u>GAT</u>	<u>ATT</u>	<u>ATC</u>	<u>GCG</u>	<u>GTT</u>	<u>GAA</u>	<u>GTA</u>	<u>AAC</u>	<u>GTG</u>	<u>GGC</u>	<u>GAC</u>	<u>ACT</u>	<u>ATT</u>	<u>GCT</u>	<u>GTG</u>	<u>GAC</u>		
124			133			142														
D	T	L	I	T	L	D	L	E												
<u>GAT</u>	<u>ACC</u>	<u>CTG</u>	<u>ATT</u>	<u>ACT</u>	<u>TTG</u>	<u>GAT</u>	<u>CTA</u>	<u>GAA</u>	<u>A</u>	3'										

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FIG. 4

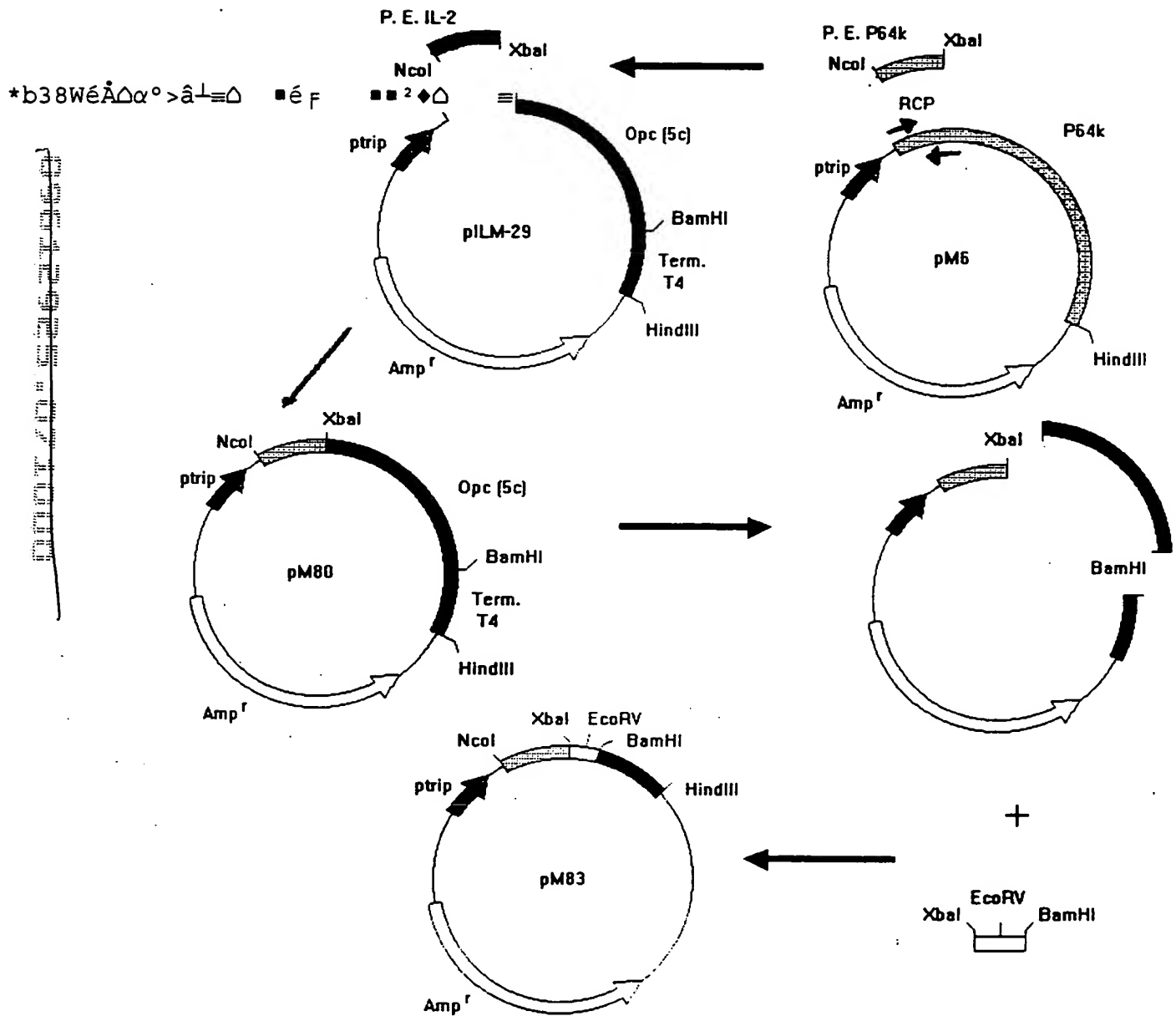


FIG. 4

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FIG. 5

Sequences producing High-scoring Segment Pairs:		High Score	Smallest Poisson Probability P(N)	N
KPY1_HUMAN	PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1...	51	0.98	1
KPY1_RAT	PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1...	51	0.98	1
KPY2_HUMAN	PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).	51	0.98	1
KPY2_RAT	PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).	51	0.98	1

>KPY1_HUMAN PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40) (CYTOSOLIC
THYROID HORMONE-BINDING PROTEIN).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

>KPY1_RAT PYRUVATE KINASE, M1 (MUSCLE) ISOZYME (EC 2.7.1.40).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

>KPY2_HUMAN PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

>KPY2_RAT PYRUVATE KINASE, M2 ISOZYME (EC 2.7.1.40).
Length = 530

Query: 29 VNVGDTIAVDDTLITLDL 46
V+VG I VDD LI+L++
Sbjct: 167 VEVGSKIYVDDGLISLQV 184

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FIG. 6

Smallest

Sequences producing High-scoring Segment Pairs:		Reading Frame	High Score	Poisson Probability P(N)	N
CFMUCIN	Canis familiaris (clone pCTM-A) mucin c-term...	-2	62	0.30	1
HS8671	EST02755 Homo sapiens cDNA clone HFBCA72 sim...	-2	61	0.40	1

>CFMUCIN Canis familiaris (clone pCTM-A) mucin c-terminus RNA, 3' end.
Length = 1733

Query: 8 LVELKVPDIGGHENVVDIIAVEVNVGDTIAVDD 39
L E+ VPD H V+++A E+ +G+++ VDD
Sbjct: 1015 LREVQVPDRKLHKGVQLLAGELGIGEALQVDD 920

>HS8671 EST02755 Homo sapiens cDNA clone HFBCA72 similar to Mucin CTM-A.
Length = 286

Query: 8 LVELKVPDIGGHENVVDIIAVEVNVGDTIAVDD 39
L E+ VPD HE V++++ E+ VG VDD
Sbjct: 240 LREVQVPDRKLHEGVQLLSGELGVGKXFQVDD 145

FIG. 7

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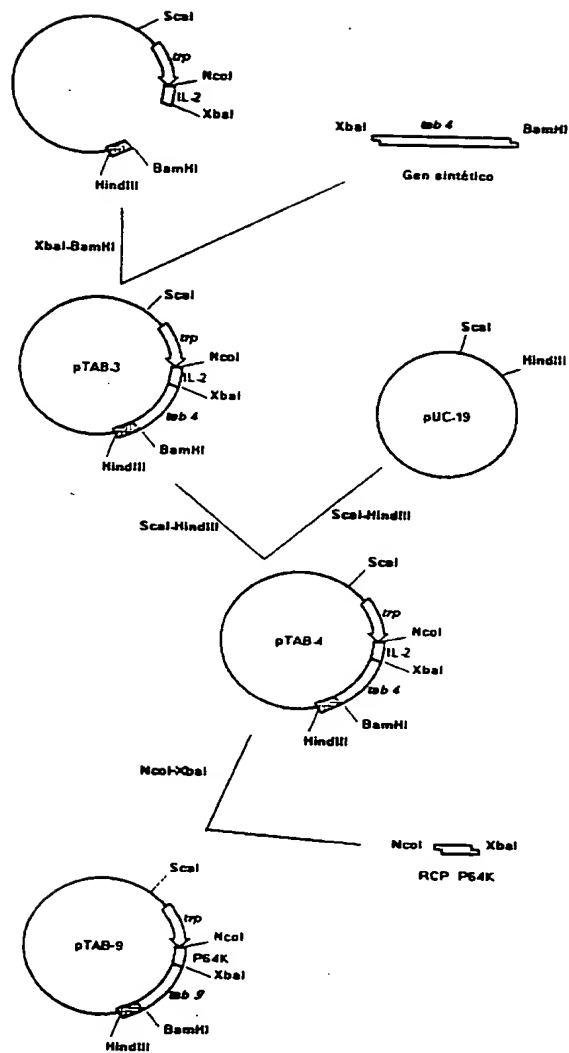


FIG. 7

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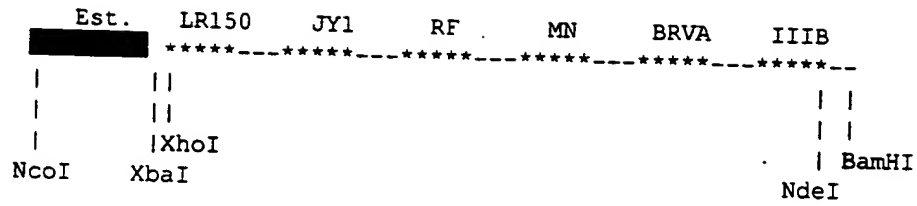
FIG. 8

			12			21			30		39			48		57		
M	V	D	K	R	M	A	L	V	E	L	K	V	P	D	I	G	G	H
ATG	GTA	GAT	AAA	AGA	ATG	GCT	TTA	GTT	GAA	TTG	AAA	GTG	CCC	GAC	ATT	GGC	GGA	CAC
			69			78			87			96			105			114
E	N	V	D	I	I	A	V	E	V	N	V	G	D	T	I	A	V	D
AA	AAT	GTA	GAT	ATT	ATC	GCG	GTT	GAA	GTA	AAC	GTG	GGC	GAC	ACT	ATT	GCT	GTG	GAC
			126			135			144			153			162			171
D	T	L	I	T	L	D	L	D	S	R	G	I	R	I	G	P	G	R
GAT	ACC	CTG	ATT	ACT	TTG	GAT	CTA	GAC	TCG	AGA	GGC	ATT	CGT	ATC	GGC	CCA	GGT	CGC
			183			192			201			210			219			228
A	I	L	A	T	A	G	G	G	A	R	Q	S	T	P	I	G	L	G
GCA	ATT	TTA	GCA	ACA	GCT	GGC	GGT	GGC	GCA	CGT	CAA	TCT	ACC	CCT	ATT	GGT	TTA	GGT
			240			249			258			267			276			285
G	A	L	Y	T	T	A	G	G	G	A	R	K	S	I	T	K	G	P
CAG	GCT	CTG	TAT	ACG	ACT	GCC	GGC	GGT	GGT	GCG	CGC	AAA	AGT	ATC	ACC	AAG	GGT	CCA
			297			306			315			324			333			342
G	R	V	I	Y	A	T	A	G	G	G	A	R	K	R	I	H	I	G
GGC	CGC	GTC	ATT	TAC	GCC	ACC	GCG	GGC	GGC	GGT	GCC	CGT	AAG	CGT	ATC	CAC	ATT	GGC
			354			363			372			381			390			399
P	G	R	A	F	Y	T	T	A	G	G	G	A	R	K	R	I	T	M
CCA	GGC	CGT	GCA	TTC	TAT	ACT	ACA	GCA	GGT	GGT	GGC	GCA	CGT	AAA	CGC	ATC	ACT	ATG
			411			420			429			438			447			456
G	P	G	R	V	Y	Y	T	T	A	G	G	G	A	S	I	R	I	Q
GGT	CCT	GGT	CGC	GTC	TAT	TAC	ACG	ACC	GCT	GGC	GGC	GGT	GCT	AGC	ATT	CGC	ATC	CAA
			468			477			486			495						
R	G	P	G	R	A	F	V	T	I	*								
CGC	GGC	CCT	GGT	CGT	GCA	TTT	GTG	ACC	ATA	TGA								

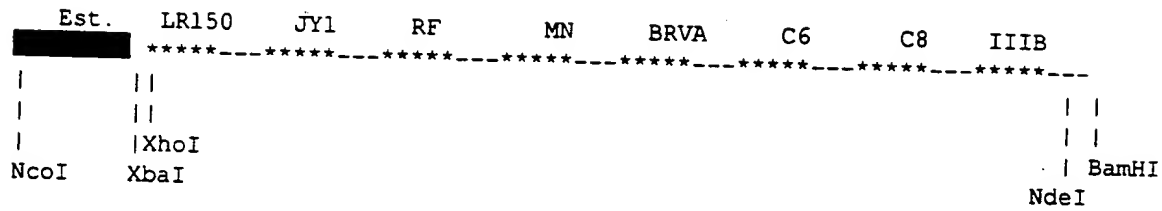
FIG. 9

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Fig. 9 A



B



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FIG. 10**A**

Gene	Strain/Vector	Plasmid	Media	Spotting Assay
<i>porA</i>	hIL2-58	pILM-28	M9	32
	P64k-47	pM-82	M9	34
<i>opc</i>	hIL2-58	pILM-29	M9	25
	P64k-47	pM-80	M9	20
TAB	hIL2-22	pTAB4	LB	5
	P64k-47	pTAB9	LB	10

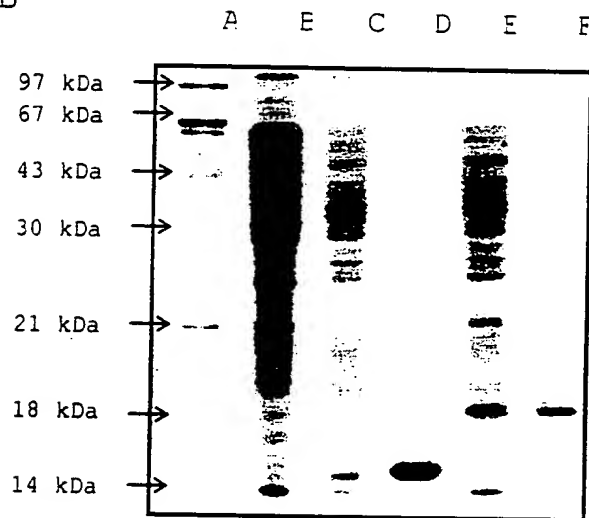
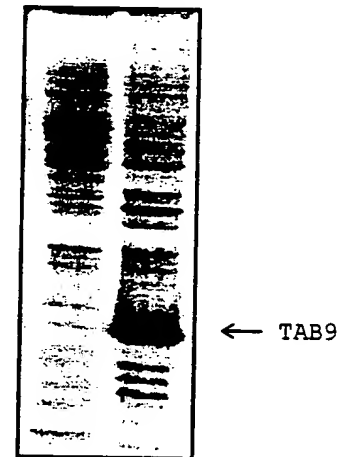
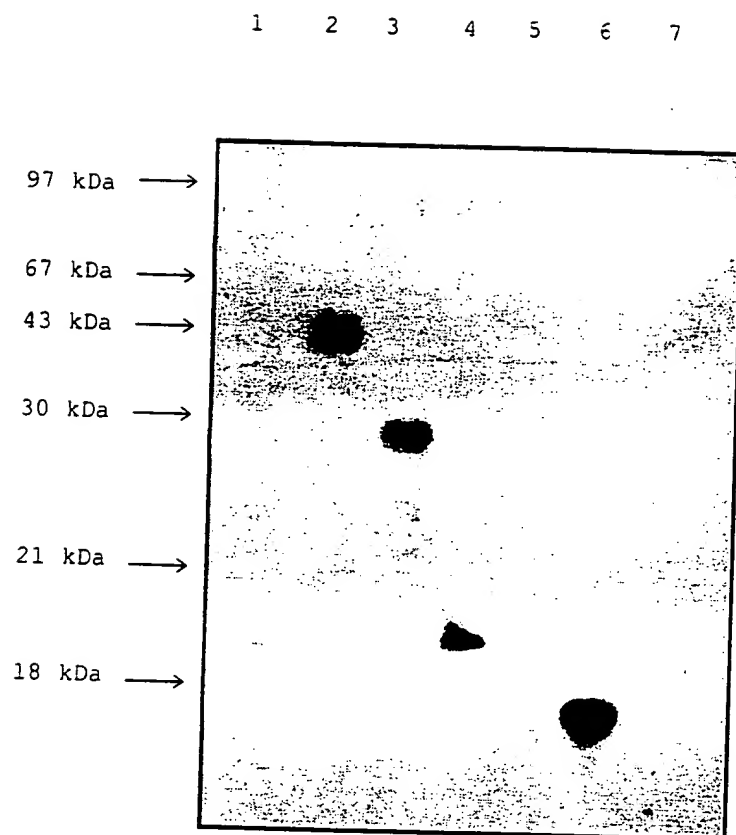
B**C**

FIG. 11

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FIG. 12

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